SEQUENCE LISTING

<110> Galloway, Susan May

Davis, George Henry

Gregan, Scott Michael

Hanrahan, James Patrick

Juengel, Jennifer Lee

McNatty, Kenneth Pattrick

Mulsant, Philippe

Powell, Richard Patrick

<120> New sequences for altering mammalian ovarian function and ovulation rate
<170> PatentIn version 3.0

<210> 1: GDF-9 [787] Full
<211> 1879
<212> DNA
<213> Ovis aries
<221> 5'UTR
<222> (1)..(121)
<221> misc_feature
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<223> atg start codon.
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<221> Intron
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<223> n at 709 represents remainder of approx 900 bp unsequenced of the approx 1.1 kb intron
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<222> (709)..()
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<221> misc_feature
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<223> taa stop codon.
<221> 3'UTR
<222> (1804)..(1879)
<221> mutation
<222> (1624)..(1626)
<223> c to t at 1625 in [787] sheep changing tct serine codon to ttt phenylalanine

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cctggttttt aggaagaaga ctggtatggg gaaatgtgtt ccttgctaat tcttccaagc
120

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    c atg gcg ctt ccc    aac aaa ttc ttc ctt    tgg ttt tgc tgc ttt    gcc
    166
      Met Ala Leu Pro    Asn Lys Phe Phe Leu    Trp Phe Cys Cys Phe    Ala
               -315               -310               -305

    tgg ctc tgt ttt    cct att agc ctt gat    tct ctg cct tct agg    gga
    211
    Trp Leu Cys Phe    Pro Ile Ser Leu Asp    Ser Leu Pro Ser Arg    Gly
             -300               -295               -290

    gaa gct cag att    gta gct agg act gcg    ttg gaa tct gag gct    gag
    256
    Glu Ala Gln Ile    Val Ala Arg Thr Ala    Leu Glu Ser Glu Ala    Glu
             -285               -280               -275

    act tgg tcc ttg    ctg aac cat tta ggt    ggg aga cac aga cct    ggt
    301
    Thr Trp Ser Leu    Leu Asn His Leu Gly    Gly Arg His Arg Pro    Gly
             -270               -265               -260

    ctc ctt tcc cct    ctc tta gag gtt ctg    tat gat ggg cac ggg    gaa
    346
    Leu Leu Ser Pro    Leu Leu Glu Val Leu    Tyr Asp Gly His Gly    Glu
             -255               -250               -245

    ccc ccc agg ctg    cag cca gat gac aga    gct ttg cgc tac atg    aag
    391
    Pro Pro Arg Leu    Gln Pro Asp Asp Arg    Ala Leu Arg Tyr Met    Lys
             -240               -235               -230

    agg ctc tat aag    gca tac gct acc aag    gag ggg acc cct aaa    tcc
    436
    Arg Leu Tyr Lys    Ala Tyr Ala Thr Lys    Glu Gly Thr Pro Lys    Ser
             -225               -220               -215

    aac aga cgc cac    ctc tac aac act gtt    cgg ctc ttc acc ccc    tgt
    481
    Asn Arg Arg His    Leu Tyr Asn Thr Val    Arg Leu Phe Thr Pro    Cys
             -210               -205               -200

    gct cag cac aag    cag gct cct ggg gac    ctg gcg gca g gtgtgtagga
    528
    Ala Gln His Lys    Gln Ala Pro Gly Asp    Leu Ala Ala
             -195               -190

    gcagattggt taatgggtgg agggaagaag aaagaccttt ttgcatttca gttacataaa
    588

    ggagttggcc ctgctccttg acttgcattt tactttgcat ggtactcaat atccaaacaa
    648

    acctggtgct tgatcttact tactgtttat tcctaatggc ctcatgggtt gatgtaggct
    708

    natcccaccc tgacgtttaa ggcttgagaa tgtggggaga aaagggacag aagcacattc
    768

    tgaggtactg attccttgat ttgacttcct gttacatatg cattactgt tggattgttt
    828

    ttcttctcag ga    acc ttt cca tca gtg gat    ctg ctg ttt aac ctg    gat
    876
                   Gly Thr    Phe Pro Ser Val Asp    Leu Leu Phe Asn Leu    Asp
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                    -185                    -180                    -175

      cgt gtt act gtt  gtg gaa cat tta ttc  aag tca gtc ttg ctg  tat
      921
 5    Arg Val Thr Val  Val Glu His Leu Phe  Lys Ser Val Leu Leu  Tyr
                -170              -165              -160


      act ttc aac aac  tcc att tct ttt ccc  ttt cct gtt aaa tgt  ata
      966
10    Thr Phe Asn Asn  Ser Ile Ser Phe Pro  Phe Pro Val Lys Cys  Ile
                -155              -150              -145


      tgc aac ctg gtg  ata aaa gag cca gag  ttt tct agc aag act  ctc
      1011
15    Cys Asn Leu Val  Ile Lys Glu Pro Glu  Phe Ser Ser Lys Thr  Leu
                -140              -135              -130


      cct aga gct cca  tac tca ttt acc tat  aac tca cag ttt gaa  ttt
      1056
20    Pro Arg Ala Pro  Tyr Ser Phe Thr Tyr  Asn Ser Gln Phe Glu  Phe
                -125              -120              -115


      aga aag aaa tac  aaa tgg atg gag att  gat gtg acg gct cct  ctt
      1101
25    Arg Lys Lys Tyr  Lys Trp Met Glu Ile  Asp Val Thr Ala Pro  Leu
                -110              -105              -100


      gag cct ctg gtg  gcc tcc cac aag agg  aat att cac atg tct gta aat
      1149
30    Glu Pro Leu Val  Ala Ser His Lys Arg  Asn Ile His Met Ser Val Asn
                -95               -90               -85


      ttt aca tgt gcg  gaa gac cag ctg cag  cat cct tca gcg cgg gac agc
      1197
35    Phe Thr Cys Ala  Glu Asp Gln Leu Gln  His Pro Ser Ala Arg Asp Ser
                -80               -75               -70


      ctg ttt aac atg  act ctt ctc gta gcg  ccc tca ctg ctt ttg tat ctg
      1245
40    Leu Phe Asn Met  Thr Leu Leu Val Ala  Pro Ser Leu Leu Leu Tyr Leu
                -65               -60               -55


      aac gac aca agt  gct cag gct ttt cac  agg tgg cat tcc ctc cac cct
      1293
45    Asn Asp Thr Ser  Ala Gln Ala Phe His  Arg Trp His Ser Leu His Pro
      -50                    -45               -40                   -35


      aaa agg aag cct  tca cag ggt cct gac  cag aag aga ggg cta tct gcc
      1341
50    Lys Arg Lys Pro  Ser Gln Gly Pro Asp  Gln Lys Arg Gly Leu Ser Ala
                -30               -25               -20


      tac ccc gtg gga  gaa gaa gct gct gag  ggt gta aga tcg tcc cgt cac
      1389
55    Tyr Pro Val Gly  Glu Glu Ala Ala Glu  Gly Val Arg Ser Ser Arg His
                -15               -10               -5


      cgc aga gac cag  gag agt gcc agc tct  gaa ttg aag aag cct ctg gtt
      1437
60    Arg Arg Asp Gln  Glu Ser Ala Ser Ser  Glu Leu Lys Lys Pro Leu Val
          -1  1                 5                 10
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cca gct tca gtc aat ctg agt gaa tac ttc aaa cag ttt ctt ttt ccc
1485
Pro Ala Ser Val Asn Leu Ser Glu Tyr Phe Lys Gln Phe Leu Phe Pro
15                  20                  25                  30

cag aat gaa tgt gag ctc cat gac ttt aga ctt agc ttt agt cag ctg
1533
Gln Asn Glu Cys Glu Leu His Asp Phe Arg Leu Ser Phe Ser Gln Leu
                35                  40                  45

aag tgg gac aac tgg att gtg gcc cca cac aaa tac aac cct cga tac
1581
Lys Trp Asp Asn Trp Ile Val Ala Pro His Lys Tyr Asn Pro Arg Tyr
            50                  55                  60

tgt aaa ggg gac tgt ccc agg gcg gtc gga cat cgg tat ggc ttt ccg
1629
Cys Lys Gly Asp Cys Pro Arg Ala Val Gly His Arg Tyr Gly Phe Pro
            65                  70                  75

gtt cac acc atg gtg cag aac atc atc cat gag aaa ctt gac tcc tca
1677
Val His Thr Met Val Gln Asn Ile Ile His Glu Lys Leu Asp Ser Ser
    80                  85                  90

gtg cca aga cca tcc tgt gta cct gcc aag tat agc cct ttg agt gtt
1725
Val Pro Arg Pro Ser Cys Val Pro Ala Lys Tyr Ser Pro Leu Ser Val
95                  100                 105                 110

ttg gcc atc gag cct gat ggc tca atc gct tat aaa gaa tat gaa gat
1773
Leu Ala Ile Glu Pro Asp Gly Ser Ile Ala Tyr Lys Glu Tyr Glu Asp
                115                 120                 125

atg ata gcc act aag tgt acc tgt cgt taacagactc ctgtcaagta
1820
Met Ile Ala Thr Lys Cys Thr Cys Arg
                130                 135

aaaccatgag tgtcctggcc agtgtaaatg ccgcgcccct gtctatgcct ttgggagga
1879
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<210> 2: protein GDF-9[787] full
<211> 453
<212> PRT
<213> Ovis aries
<221> misc_feature
<222> (122)..(124)
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<223> n represents approximately 900 bp of unsequenced intron
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<222> (1801)..(1803)
<223> taa stop codon.

<400> 2

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Met Ala Leu Pro   Asn Lys Phe Phe   Leu Trp Phe Cys   Cys Phe Ala
         -315   -310   -305

Trp Leu Cys Phe   Pro Ile Ser Leu   Asp Ser Leu Pro   Ser Arg Gly
         -300   -295   -290

10

Glu Ala Gln Ile   Val Ala Arg Thr   Ala Leu Glu Ser   Glu Ala Glu
         -285   -280   -275

15 Thr Trp Ser Leu   Leu Asn His Leu   Gly Gly Arg His   Arg Pro Gly
             -270   -265   -260

20 Leu Leu Ser Pro   Leu Leu Glu Val   Leu Tyr Asp Gly   His Gly Glu
             -255   -250   -245

Pro Pro Arg Leu   Gln Pro Asp Asp   Arg Ala Leu Arg   Tyr Met Lys
         -240   -235   -230

25

Arg Leu Tyr Lys   Ala Tyr Ala Thr   Lys Glu Gly Thr   Pro Lys Ser
         -225   -220   -215

30

Asn Arg Arg His   Leu Tyr Asn Thr   Val Arg Leu Phe   Thr Pro Cys
         -210   -205   -200

35 Ala Gln His Lys   Gln Ala Pro Gly   Asp Leu Ala Ala   Gly Thr Phe
             -195   -190   -185

Pro Ser Val Asp   Leu Leu Phe Asn   Leu Asp Arg Val   Thr Val Val
         -180   -175   -170

40

Glu His Leu Phe   Lys Ser Val Leu   Leu Tyr Thr Phe   Asn Asn Ser
         -165   -160   -155

45

Ile Ser Phe Pro   Phe Pro Val Lys   Cys Ile Cys Asn   Leu Val Ile
         -150   -145   -140

50

Lys Glu Pro Glu   Phe Ser Ser Lys   Thr Leu Pro Arg   Ala Pro Tyr
         -135   -130   -125

55 Ser Phe Thr Tyr   Asn Ser Gln Phe   Glu Phe Arg Lys   Lys Tyr Lys
             -120   -115   -110

60 Trp Met Glu Ile   Asp Val Thr Ala   Pro Leu Glu Pro   Leu Val Ala Ser
             -105   -100   -95

● ●

6

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        His Lys Arg Asn Ile His Met Ser Val Asn Phe Thr Cys Ala Glu Asp
                -90                 -85             -80


 5      Gln Leu Gln His Pro Ser Ala Arg Asp Ser Leu Phe Asn Met Thr Leu
                -75             -70             -65


        Leu Val Ala Pro Ser Leu Leu Leu Tyr Leu Asn Asp Thr Ser Ala Gln
10      -60             -55             -50                     -45


        Ala Phe His Arg Trp His Ser Leu His Pro Lys Arg Lys Pro Ser Gln
                        -40             -35                     -30
15

        Gly Pro Asp Gln Lys Arg Gly Leu Ser Ala Tyr Pro Val Gly Glu Glu
                    -25             -20             -15

20
        Ala Ala Glu Gly Val Arg Ser Ser Arg His Arg Arg Asp Gln Glu Ser
                -10                 -5                 -1  1


25      Ala Ser Ser Glu Leu Lys Lys Pro Leu Val Pro Ala Ser Val Asn Leu
        5                   10              15                      20


        Ser Glu Tyr Phe Lys Gln Phe Leu Phe Pro Gln Asn Glu Cys Glu Leu
30                      25              30                  35


        His Asp Phe Arg Leu Ser Phe Ser Gln Leu Lys Trp Asp Asn Trp Ile
                    40              45                  50
35

        Val Ala Pro His Lys Tyr Asn Pro Arg Tyr Cys Lys Gly Asp Cys Pro
                55                  60                  65
40

        Arg Ala Val Gly His Arg Tyr Gly Phe Pro Val His Thr Met Val Gln
                70                  75                  80


45      Asn Ile Ile His Glu Lys Leu Asp Ser Ser Val Pro Arg Pro Ser Cys
        85                  90                  95                  100


        Val Pro Ala Lys Tyr Ser Pro Leu Ser Val Leu Ala Ile Glu Pro Asp
50                      105             110                 115


        Gly Ser Ile Ala Tyr Lys Glu Tyr Glu Asp Met Ile Ala Thr Lys Cys
                    120             125                 130
55

        Thr Cys Arg
                135

60
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<210>  3: GDF-9 [787] coding
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<212>  DNA
<213>  Ovis aries
<221>  misc_feature
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<222>  (1)..(1359)
<221>  mat_peptide
<222>  (955)..()
<221>  mutation
<222>  (1183)..(1185)
<223>  c to t 1184 in [787] sheep changing serine tct codon to ttt
phenylalanine
<221>  misc_feature
<222>  (1360)..(1362)
<223>  taa stop codon.

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Met Ala Leu Pro  Asn Lys Phe Phe Leu  Trp Phe Cys Cys Phe  Ala
            -315              -310              -305


tgg ctc tgt ttt  cct att agc ctt gat  tct ctg cct tct agg  gga
90
Trp Leu Cys Phe  Pro Ile Ser Leu Asp  Ser Leu Pro Ser Arg  Gly
            -300              -295              -290


gaa gct cag att  gta gct agg act gcg  ttg gaa tct gag gct  gag
135
Glu Ala Gln Ile  Val Ala Arg Thr Ala  Leu Glu Ser Glu Ala  Glu
            -285              -280              -275


act tgg tcc ttg  ctg aac cat tta ggt  ggg aga cac aga cct  ggt
180
Thr Trp Ser Leu  Leu Asn His Leu Gly  Gly Arg His Arg Pro  Gly
            -270              -265              -260


ctc ctt tcc cct  ctc tta gag gtt ctg  tat gat ggg cac ggg  gaa
225
Leu Leu Ser Pro  Leu Leu Glu Val Leu  Tyr Asp Gly His Gly  Glu
            -255              -250              -245


ccc ccc agg ctg  cag cca gat gac aga  gct ttg cgc tac atg  aag
270
Pro Pro Arg Leu  Gln Pro Asp Asp Arg  Ala Leu Arg Tyr Met  Lys
            -240              -235              -230


agg ctc tat aag  gca tac gct acc aag  gag ggg acc cct aaa  tcc
315
Arg Leu Tyr Lys  Ala Tyr Ala Thr Lys  Glu Gly Thr Pro Lys  Ser
            -225              -220              -215


aac aga cgc cac  ctc tac aac act gtt  cgg ctc ttc acc ccc  tgt
360
Asn Arg Arg His  Leu Tyr Asn Thr Val  Arg Leu Phe Thr Pro  Cys
            -210              -205              -200


gct cag cac aag  cag gct cct ggg gac  ctg gcg gca gga acc  ttt
405
Ala Gln His Lys  Gln Ala Pro Gly Asp  Leu Ala Ala Gly Thr  Phe
```

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                    -195                    -190                    -185

       cca tca gtg gat   ctg ctg ttt aac   ctg   gat cgt gtt act   gtt   gtg
       450
5      Pro Ser Val Asp   Leu Leu Phe Asn   Leu   Asp Arg Val Thr   Val   Val
                    -180                    -175                    -170

       gaa cat tta ttc   aag tca gtc ttg   ctg   tat act ttc aac   aac   tcc
       495
10     Glu His Leu Phe   Lys Ser Val Leu   Leu   Tyr Thr Phe Asn   Asn   Ser
                    -165                    -160                    -155

       att tct ttt ccc   ttt cct gtt aaa   tgt   ata tgc aac ctg   gtg   ata
       540
15     Ile Ser Phe Pro   Phe Pro Val Lys   Cys   Ile Cys Asn Leu   Val   Ile
                    -150                    -145                    -140

       aaa gag cca gag   ttt tct agc aag   act   ctc cct aga gct   cca   tac
       585
20     Lys Glu Pro Glu   Phe Ser Ser Lys   Thr   Leu Pro Arg Ala   Pro   Tyr
                    -135                    -130                    -125

       tca ttt acc tat   aac tca cag ttt   gaa   ttt aga aag aaa   tac   aaa
       630
25     Ser Phe Thr Tyr   Asn Ser Gln Phe   Glu   Phe Arg Lys Lys   Tyr   Lys
                    -120                    -115                    -110

       tgg atg gag att   gat gtg acg gct   cct   ctt gag cct ctg gtg gcc tcc
       678
30     Trp Met Glu Ile   Asp Val Thr Ala   Pro   Leu Glu Pro Leu Val Ala Ser
                    -105                    -100                    -95

       cac aag agg aat att cac atg tct gta aat ttt aca tgt gcg gaa gac
       726
35     His Lys Arg Asn Ile His Met Ser Val Asn Phe Thr Cys Ala Glu Asp
                -90                 -85                 -80

       cag ctg cag cat cct tca gcg cgg gac agc ctg ttt aac atg act ctt
       774
40     Gln Leu Gln His Pro Ser Ala Arg Asp Ser Leu Phe Asn Met Thr Leu
              -75                 -70                 -65

       ctc gta gcg ccc tca ctg ctt ttg tat ctg aac gac aca agt gct cag
       822
45     Leu Val Ala Pro Ser Leu Leu Leu Tyr Leu Asn Asp Thr Ser Ala Gln
       -60                 -55                 -50                 -45

       gct ttt cac agg tgg cat tcc ctc cac cct aaa agg aag cct tca cag
       870
50     Ala Phe His Arg Trp His Ser Leu His Pro Lys Arg Lys Pro Ser Gln
                      -40                 -35                 -30

       ggt cct gac cag aag aga ggg cta tct gcc tac ccc gtg gga gaa gaa
       918
55     Gly Pro Asp Gln Lys Arg Gly Leu Ser Ala Tyr Pro Val Gly Glu Glu
                -25                 -20                 -15

       gct gct gag ggt gta aga tcg tcc cgt cac cgc aga gac cag gag agt
       966
60     Ala Ala Glu Gly Val Arg Ser Ser Arg His Arg Arg Asp Gln Glu Ser
                -10                 -5                  -1  1
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gcc agc tct gaa ttg aag aag cct ctg gtt cca gct tca gtc aat ctg
1014
Ala Ser Ser Glu Leu Lys Lys Pro Leu Val Pro Ala Ser Val Asn Leu
5   10   15   20

agt gaa tac ttc aaa cag ttt ctt ttt ccc cag aat gaa tgt gag ctc
1062
Ser Glu Tyr Phe Lys Gln Phe Leu Phe Pro Gln Asn Glu Cys Glu Leu
          25   30   35

cat gac ttt aga ctt agc ttt agt cag ctg aag tgg gac aac tgg att
1110
His Asp Phe Arg Leu Ser Phe Ser Gln Leu Lys Trp Asp Asn Trp Ile
          40   45   50

gtg gcc cca cac aaa tac aac cct cga tac tgt aaa ggg gac tgt ccc
1158
Val Ala Pro His Lys Tyr Asn Pro Arg Tyr Cys Lys Gly Asp Cys Pro
          55   60   65

agg gcg gtc gga cat cgg tat ggc ttt ccg gtt cac acc atg gtg cag
1206
Arg Ala Val Gly His Arg Tyr Gly Phe Pro Val His Thr Met Val Gln
    70   75   80

aac atc atc cat gag aaa ctt gac tcc tca gtg cca aga cca tcc tgt
1254
Asn Ile Ile His Glu Lys Leu Asp Ser Ser Val Pro Arg Pro Ser Cys
85   90   95   100

gta cct gcc aag tat agc cct ttg agt gtt ttg gcc atc gag cct gat
1302
Val Pro Ala Lys Tyr Ser Pro Leu Ser Val Leu Ala Ile Glu Pro Asp
          105   110   115

ggc tca atc gct tat aaa gaa tat gaa gat atg ata gcc act aag tgt
1350
Gly Ser Ile Ala Tyr Lys Glu Tyr Glu Asp Met Ile Ala Thr Lys Cys
          120   125   130

acc tgt cgt taa
1362
Thr Cys Arg
          135

<210>   4: Protein GDF-9 [787] coding
<211>   453
<212>   PRT
<213>   Ovis aries
<221>   misc_feature
<222>   (1)..(3)
<223>   atg start codon.
<221>   misc_feature
<222>   (1360)..(1362)
<223>   taa stop codon.

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Met Ala Leu Pro Asn Lys Phe Phe Leu Trp Phe Cys Cys Phe Ala
          -315   -310   -305

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      Trp Leu Cys Phe  Pro Ile Ser Leu Asp  Ser Leu Pro Ser Arg  Gly
                -300              -295                  -290

 5    Glu Ala Gln Ile  Val Ala Arg Thr Ala  Leu Glu Ser Glu Ala  Glu
                -285              -280                  -275

10    Thr Trp Ser Leu  Leu Asn His Leu Gly  Gly Arg His Arg Pro  Gly
                -270              -265                  -260

      Leu Leu Ser Pro  Leu Leu Glu Val Leu  Tyr Asp Gly His Gly  Glu
                -255              -250                  -245
15

      Pro Pro Arg Leu  Gln Pro Asp Asp Arg  Ala Leu Arg Tyr Met  Lys
                -240              -235                  -230
20

      Arg Leu Tyr Lys  Ala Tyr Ala Thr Lys  Glu Gly Thr Pro Lys  Ser
                -225              -220                  -215

25    Asn Arg Arg His  Leu Tyr Asn Thr Val  Arg Leu Phe Thr Pro  Cys
                -210              -205                  -200

      Ala Gln His Lys  Gln Ala Pro Gly Asp  Leu Ala Ala Gly Thr  Phe
30              -195              -190                  -185

      Pro Ser Val Asp  Leu Leu Phe Asn Leu  Asp Arg Val Thr Val  Val
                -180              -175                  -170
35

      Glu His Leu Phe  Lys Ser Val Leu Leu  Tyr Thr Phe Asn Asn  Ser
                -165              -160                  -155
40

      Ile Ser Phe Pro  Phe Pro Val Lys Cys  Ile Cys Asn Leu Val  Ile
                -150              -145                  -140

45    Lys Glu Pro Glu  Phe Ser Ser Lys Thr  Leu Pro Arg Ala Pro  Tyr
                -135              -130                  -125

      Ser Phe Thr Tyr  Asn Ser Gln Phe Glu  Phe Arg Lys Lys Tyr  Lys
50              -120              -115                  -110

      Trp Met Glu Ile  Asp Val Thr Ala Pro  Leu Glu Pro Leu Val Ala Ser
                -105              -100                  -95
55

      His Lys Arg Asn  Ile His Met Ser Val  Asn Phe Thr Cys Ala Glu Asp
                -90                 -85                  -80
60

      Gln Leu Gln His  Pro Ser Ala Arg Asp  Ser Leu Phe Asn Met Thr Leu
           -75                 -70                  -65
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     Leu Val Ala Pro Ser Leu Leu Leu Tyr Leu Asn Asp Thr Ser Ala Gln
     -60             -55             -50                         -45

5

     Ala Phe His Arg Trp His Ser Leu His Pro Lys Arg Lys Pro Ser Gln
                 -40             -35                         -30

10

     Gly Pro Asp Gln Lys Arg Gly Leu Ser Ala Tyr Pro Val Gly Glu Glu
                 -25             -20                 -15

15   Ala Ala Glu Gly Val Arg Ser Ser Arg His Arg Arg Asp Gln Glu Ser
                 -10              -5              -1  1

     Ala Ser Ser Glu Leu Lys Lys Pro Leu Val Pro Ala Ser Val Asn Leu
20   5                   10                  15                  20

     Ser Glu Tyr Phe Lys Gln Phe Leu Phe Pro Gln Asn Glu Cys Glu Leu
25                   25                  30                  35

     His Asp Phe Arg Leu Ser Phe Ser Gln Leu Lys Trp Asp Asn Trp Ile
30                40                  45                  50

     Val Ala Pro His Lys Tyr Asn Pro Arg Tyr Cys Lys Gly Asp Cys Pro
                 55                  60                  65

35   Arg Ala Val Gly His Arg Tyr Gly Phe Pro Val His Thr Met Val Gln
         70                  75                  80

     Asn Ile Ile His Glu Lys Leu Asp Ser Ser Val Pro Arg Pro Ser Cys
40   85                  90                  95                  100

     Val Pro Ala Lys Tyr Ser Pro Leu Ser Val Leu Ala Ile Glu Pro Asp
                 105                 110                 115

45

     Gly Ser Ile Ala Tyr Lys Glu Tyr Glu Asp Met Ile Ala Thr Lys Cys
                 120                 125                 130

50

     Thr Cys Arg
                 135


55   <210>   5: GDF-9 [787] mutation
     <211>   168
     <212>   DNA
     <213>   Ovis aries
     <221>   CDS
60   <222>   (1)..(168)
     <221>   mutation
     <222>   (82)..(84)
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<223> c to t at 83 in [787] sheep changing tct serine codon to ttt phenylalanine

<400> 5
aac tgg att gtg gcc cca cac aaa tac aac cct cga tac tgt aaa ggg
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Asn Trp Ile Val Ala Pro His Lys Tyr Asn Pro Arg Tyr Cys Lys Gly
1   5   10   15

gac tgt ccc agg gcg gtc gga cat cgg tat ggc ttt ccg gtt cac acc
96
Asp Cys Pro Arg Ala Val Gly His Arg Tyr Gly Phe Pro Val His Thr
            20   25   30

atg gtg cag aac atc atc cat gag aaa ctt gac tcc tca gtg cca aga
144
Met Val Gln Asn Ile Ile His Glu Lys Leu Asp Ser Ser Val Pro Arg
        35   40   45

cca tcc tgt gta cct gcc aag tat
168
Pro Ser Cys Val Pro Ala Lys Tyr
    50   55

<210>   6: protein GDF-9 [787] mutation
<211>   56
<212>   PRT
<213>   Ovis aries

<400>   6

Asn Trp Ile Val Ala Pro His Lys Tyr Asn Pro Arg Tyr Cys Lys Gly
1   5   10   15

Asp Cys Pro Arg Ala Val Gly His Arg Tyr Gly Phe Pro Val His Thr
            20   25   30

Met Val Gln Asn Ile Ile His Glu Lys Leu Asp Ser Ser Val Pro Arg
        35   40   45

Pro Ser Cys Val Pro Ala Lys Tyr
    50   55

<210>   7: GDF-9B [S1] full
<211>   1665
<212>   DNA
<213>   Ovis aries
<221>   5'UTR
<222>   (1)..(252)
<221>   misc_feature
<222>   (253)..(255)
<223>   atg start codon.
<221>   CDS
<222>   (253)..(577)
<221>   CDS
<222>   (774)..(1165)
<221>   Intron
<222>   (578)..(773)

```
<223>  n at 685 represents remainder of approx 5.2 kb intron.
<221>  misc_feature
<222>  (1253)..(1255)
<223>  position of first codon of mature peptide in wildtype sheep.
<221>  misc_feature
<222>  (685)..()
<223>  n represents approx 5.2 kb of intron.
<221>  misc_feature
<222>  (1628)..(1630)
<223>  tga stop codon in wildtype sheep.
<221>  3'UTR
<222>  (1631)..(1665)
<221>  mutation
<222>  (1166)..(1168)
<223>  c to t at 1166 of [S1] sheep changes cag glutamine codon to tag
STOP
```

```
<400>  7
catgctgcct tgtcccacct gctgtttctg tttgtttgat gcaaagagga caatttagaa
60

gacctctttt tggttcagga gatcctacca gaggaagaaa cataggacct gcctgccagc
120

ctttcatttt tccttgccct atcctttgtg gtagtggagc ctggatgctg ttacccatgt
180

aaaaggaaag gtttaaagcg ttatcctttg ggcttttatc agaacatgtt gctgaacacc
240

aagctttca ag atg gtc ctc ctg agc atc ctt aga atc ctt ctt tgg gga
291
            Met Val Leu Leu Ser Ile Leu Arg Ile Leu Leu Trp Gly
            1               5                   10

ctg gtg ctt ttt atg gaa cat agg gtc caa atg aca cag gta ggg cag
339
Leu Val Leu Phe Met Glu His Arg Val Gln Met Thr Gln Val Gly Gln
    15                  20                  25

ccc tct att gcc cac ctg cct gag gcc cct acc ttg ccc ctg att cag
387
Pro Ser Ile Ala His Leu Pro Glu Ala Pro Thr Leu Pro Leu Ile Gln
30                  35                  40                  45

gag ctg cta gaa gaa gcc cct ggc aag cag cag agg aag ccg cgg gtc
435
Glu Leu Leu Glu Glu Ala Pro Gly Lys Gln Gln Arg Lys Pro Arg Val
                50                  55                  60

tta ggg cat ccc tta cgg tat atg ctg gag ctg tac cag cgt tca gct
483
Leu Gly His Pro Leu Arg Tyr Met Leu Glu Leu Tyr Gln Arg Ser Ala
            65                  70                  75

gac gca agt gga cac cct agg gaa aac cgc acc att ggg gcc acc atg
531
Asp Ala Ser Gly His Pro Arg Glu Asn Arg Thr Ile Gly Ala Thr Met
            80                  85                  90

gtg agg ctg gtg agg ccg ctg gct agt gta gca agg cct ctc aga g
577
```

```
          Val Arg Leu Val Arg Pro Leu Ala Ser Val Ala Arg Pro Leu Arg
               95                  100                  105
```

```
5    gtgagttatc atactatatt gttctggtgg gaggggggga gaaatggggg aagaaaagtg
     637
```

```
     tagaaaaaag tggatctgtc agttttctgt caggcttcac attgcctnca gtttgtactg
     697
```

```
10   agcaggtctg ttagagagac taaggctagg atataagaag ctaacgcttt gctcttgttc
     757
```

```
     cctcttacta atgcag gc  tcc tgg cac ata cag acc ctg gac ttt cct ctg
     808
15                       Gly Ser Trp His Ile Gln Thr Leu Asp Phe Pro Leu
                         110                  115                  120
```

```
     aga cca aac cgg gta gca tac caa cta gtc aga gcc act gtg gtt tac
     856
20   Arg Pro Asn Arg Val Ala Tyr Gln Leu Val Arg Ala Thr Val Val Tyr
                         125                  130                  135
```

```
     cgc cat cag ctt cac cta act cat tcc cac ctc tcc tgc cat gtg gag
     904
25   Arg His Gln Leu His Leu Thr His Ser His Leu Ser Cys His Val Glu
                         140                  145                  150
```

```
     ccc tgg gtc cag aaa agc cca acc aat cac ttt cct tct tca gga aga
     952
30   Pro Trp Val Gln Lys Ser Pro Thr Asn His Phe Pro Ser Ser Gly Arg
                     155                  160                  165
```

```
     ggc tcc tca aag cct tcc ctg ttg ccc aaa act tgg aca gag atg gat
     1000
35   Gly Ser Ser Lys Pro Ser Leu Leu Pro Lys Thr Trp Thr Glu Met Asp
                 170                  175                  180
```

```
     atc atg gaa cat gtt ggg caa aag ctc tgg aat cac aag ggg cgc agg
     1048
40   Ile Met Glu His Val Gly Gln Lys Leu Trp Asn His Lys Gly Arg Arg
     185                  190                  195                  200
```

```
     gtt cta cga ctc cgc ttc gtg tgt cag cag cca aga ggt agt gag gtt
     1096
45   Val Leu Arg Leu Arg Phe Val Cys Gln Gln Pro Arg Gly Ser Glu Val
                     205                  210                  215
```

```
     ctt gag ttc tgg tgg cat ggc act tca tca ttg gac act gtc ttc ttg
     1144
50   Leu Glu Phe Trp Trp His Gly Thr Ser Ser Leu Asp Thr Val Phe Leu
                     220                  225                  230
```

```
     tta ctg tat ttc aat gac act tagagtgttc agaagaccaa acctctccct
     1195
55   Leu Leu Tyr Phe Asn Asp Thr
                     235
```

```
     aaaggcctga aagagtttac agaaaaagac ccttctcttc tcttgaggag ggctcgtcaa
     1255
60
```

```
     gcaggcagta ttgcatcgga agttcctggc ccctccaggg agcatgatgg gcctgaaagt
     1315
```

aaccagtgtt ccctccaccc ttttcaagtc agcttccagc agctgggctg ggatcactgg
1375

atcattgctc cccatctcta taccccaaac tactgtaagg gagtatgtcc tcgggtacta
1435

cactatggtc tcaattctcc caatcatgcc atcatccaga accttgtcag tgagctggtg
1495

gatcagaatg tccctcagcc ttcctgtgtc ccttataagt atgttcccat tagcatcctt
1555

ctgattgagg caaatgggag tatcttgtac aaggagtatg agggtatgat tgcccagtcc
1615

tgcacatgca ggtgacggca aaggtgcagc tagctcaggt ttcccaagaa
1665

<210> 8: protein GDF-9B [S1] full
<211> 239
<212> PRT
<213> Ovis aries
<221> misc_feature
<222> (253)..(255)
<223> atg start codon.
<221> misc_feature
<222> (1253)..(1255)
<223> position of first codon of mature peptide in wildtype sheep.
<221> misc_feature
<222> (685)..()
<223> n represents approx 5.2 kb of intron.
<221> misc_feature
<222> (1628)..(1630)
<223> tga stop codon in wildtype sheep.

<400> 8

Met Val Leu Leu Ser Ile Leu Arg Ile Leu Leu Trp Gly Leu Val Leu
1   5   10   15

Phe Met Glu His Arg Val Gln Met Thr Gln Val Gly Gln Pro Ser Ile
            20   25   30

Ala His Leu Pro Glu Ala Pro Thr Leu Pro Leu Ile Gln Glu Leu Leu
        35   40   45

Glu Glu Ala Pro Gly Lys Gln Gln Arg Lys Pro Arg Val Leu Gly His
    50   55   60

Pro Leu Arg Tyr Met Leu Glu Leu Tyr Gln Arg Ser Ala Asp Ala Ser
65   70   75   80

Gly His Pro Arg Glu Asn Arg Thr Ile Gly Ala Thr Met Val Arg Leu
                85   90   95

```
        Val Arg Pro Leu Ala Ser Val Ala Arg Pro Leu Arg Gly Ser Trp His
                    100                 105                 110
```

5
```
        Ile Gln Thr Leu Asp Phe Pro Leu Arg Pro Asn Arg Val Ala Tyr Gln
                    115                 120                 125
```

```
        Leu Val Arg Ala Thr Val Val Tyr Arg His Gln Leu His Leu Thr His
10          130                 135                 140
```

```
        Ser His Leu Ser Cys His Val Glu Pro Trp Val Gln Lys Ser Pro Thr
        145                 150                 155                 160
15
```

```
        Asn His Phe Pro Ser Ser Gly Arg Gly Ser Ser Lys Pro Ser Leu Leu
                    165                 170                 175
20
```

```
        Pro Lys Thr Trp Thr Glu Met Asp Ile Met Glu His Val Gly Gln Lys
                    180                 185                 190
```

25
```
        Leu Trp Asn His Lys Gly Arg Arg Val Leu Arg Leu Arg Phe Val Cys
                    195                 200                 205
```

```
        Gln Gln Pro Arg Gly Ser Glu Val Leu Glu Phe Trp Trp His Gly Thr
30          210                 215                 220
```

```
        Ser Ser Leu Asp Thr Val Phe Leu Leu Leu Tyr Phe Asn Asp Thr
        225                 230                 235
35
```

```
<210>   9: GDF-9B [S1] coding
<211>   1182
<212>   DNA
40  <213>   Ovis areis
<221>   misc_feature
<222>   (1)..(3)
<223>   atg start codon
<221>   mutation
45  <222>   (718)..(720)
<223>   c to t at 718 of [S1] sheep changes cag glutamine codon to tag
STOP.
<221>   CDS
<222>   (1)..(717)
50  <221>   misc_feature
<222>   (805)..(807)
<223>   first codon of mature peptide in wildtype sheep.
<221>   misc_feature
<222>   (1180)..(1182)
55  <223>   tga stop codon.

<400>   9
atg gtc ctc ctg agc atc ctt aga atc ctt ctt tgg gga ctg gtg ctt
48
60  Met Val Leu Leu Ser Ile Leu Arg Ile Leu Leu Trp Gly Leu Val Leu
    1               5                   10                  15
```

```
ttt atg gaa cat agg gtc caa atg aca cag gta ggg cag ccc tct att
96
Phe Met Glu His Arg Val Gln Met Thr Gln Val Gly Gln Pro Ser Ile
        20              25              30

gcc cac ctg cct gag gcc cct acc ttg ccc ctg att cag gag ctg cta
144
Ala His Leu Pro Glu Ala Pro Thr Leu Pro Leu Ile Gln Glu Leu Leu
        35              40              45

gaa gaa gcc cct ggc aag cag cag agg aag ccg cgg gtc tta ggg cat
192
Glu Glu Ala Pro Gly Lys Gln Gln Arg Lys Pro Arg Val Leu Gly His
    50              55              60

ccc tta cgg tat atg ctg gag ctg tac cag cgt tca gct gac gca agt
240
Pro Leu Arg Tyr Met Leu Glu Leu Tyr Gln Arg Ser Ala Asp Ala Ser
65              70              75              80

gga cac cct agg gaa aac cgc acc att ggg gcc acc atg gtg agg ctg
288
Gly His Pro Arg Glu Asn Arg Thr Ile Gly Ala Thr Met Val Arg Leu
            85              90              95

gtg agg ccg ctg gct agt gta gca agg cct ctc aga ggc tcc tgg cac
336
Val Arg Pro Leu Ala Ser Val Ala Arg Pro Leu Arg Gly Ser Trp His
        100             105             110

ata cag acc ctg gac ttt cct ctg aga cca aac cgg gta gca tac caa
384
Ile Gln Thr Leu Asp Phe Pro Leu Arg Pro Asn Arg Val Ala Tyr Gln
        115             120             125

cta gtc aga gcc act gtg gtt tac cgc cat cag ctt cac cta act cat
432
Leu Val Arg Ala Thr Val Val Tyr Arg His Gln Leu His Leu Thr His
    130             135             140

tcc cac ctc tcc tgc cat gtg gag ccc tgg gtc cag aaa agc cca acc
480
Ser His Leu Ser Cys His Val Glu Pro Trp Val Gln Lys Ser Pro Thr
145             150             155             160

aat cac ttt cct tct tca gga aga ggc tcc tca aag cct tcc ctg ttg
528
Asn His Phe Pro Ser Ser Gly Arg Gly Ser Ser Lys Pro Ser Leu Leu
                165             170             175

ccc aaa act tgg aca gag atg gat atc atg gaa cat gtt ggg caa aag
576
Pro Lys Thr Trp Thr Glu Met Asp Ile Met Glu His Val Gly Gln Lys
        180             185             190

ctc tgg aat cac aag ggg cgc agg gtt cta cga ctc cgc ttc gtg tgt
624
Leu Trp Asn His Lys Gly Arg Arg Val Leu Arg Leu Arg Phe Val Cys
        195             200             205

cag cag cca aga ggt agt gag gtt ctt gag ttc tgg tgg cat ggc act
672
```

```
    Gln Gln Pro Arg Gly Ser Glu Val Leu Glu Phe Trp Trp His Gly Thr
        210             215             220
```

```
5   tca tca ttg gac act gtc ttc ttg tta ctg tat ttc aat gac act
    717
    Ser Ser Leu Asp Thr Val Phe Leu Leu Leu Tyr Phe Asn Asp Thr
    225             230             235
```

```
10  tagagtgttc agaagaccaa acctctccct aaaggcctga aagagtttac agaaaaagac
    777
```

```
    ccttctcttc tcttgaggag ggctcgtcaa gcaggcagta ttgcatcgga agttcctggc
    837
```

```
15  ccctccaggg agcatgatgg gcctgaaagt aaccagtgtt ccctccaccc ttttcaagtc
    897
```

```
    agcttccagc agctgggctg ggatcactgg atcattgctc cccatctcta taccccaaac
    957
```

```
20  tactgtaagg gagtatgtcc tcgggtacta cactatggtc tcaattctcc caatcatgcc
    1017
```

```
25  atcatccaga accttgtcag tgagctggtg gatcagaatg tccctcagcc ttcctgtgtc
    1077
```

```
    ccttataagt atgttcccat tagcatcctt ctgattgagg caaatgggag tatcttgtac
    1137
```

```
30  aaggagtatg agggtatgat tgcccagtcc tgcacatgca ggtga
    1182
```

```
    <210>  10: protein GDF-9B [S1] coding
35  <211>  239
    <212>  PRT
    <213>  Ovis areis
    <221>  misc_feature
    <222>  (1)..(3)
40  <223>  atg start codon.
    <221>  misc_feature
    <222>  (805)..(807)
    <223>  first codon of mature peptide in wildtype sheep.
    <221>  misc_feature
45  <222>  (1180)..(1182)
    <223>  tga stop codon.
```

```
    <400>  10
```

```
50  Met Val Leu Leu Ser Ile Leu Arg Ile Leu Leu Trp Gly Leu Val Leu
    1               5                   10                  15
```

```
55  Phe Met Glu His Arg Val Gln Met Thr Gln Val Gly Gln Pro Ser Ile
                20                  25                  30
```

```
    Ala His Leu Pro Glu Ala Pro Thr Leu Pro Leu Ile Gln Glu Leu Leu
                35                  40                  45
60
```

```
    Glu Glu Ala Pro Gly Lys Gln Gln Arg Lys Pro Arg Val Leu Gly His
        50              55                  60
```

```
      Pro Leu Arg Tyr Met Leu Glu Leu Tyr Gln Arg Ser Ala Asp Ala Ser
      65              70              75              80

      Gly His Pro Arg Glu Asn Arg Thr Ile Gly Ala Thr Met Val Arg Leu
                  85              90              95

      Val Arg Pro Leu Ala Ser Val Ala Arg Pro Leu Arg Gly Ser Trp His
                  100             105             110

      Ile Gln Thr Leu Asp Phe Pro Leu Arg Pro Asn Arg Val Ala Tyr Gln
                  115             120             125

      Leu Val Arg Ala Thr Val Val Tyr Arg His Gln Leu His Leu Thr His
          130             135             140

      Ser His Leu Ser Cys His Val Glu Pro Trp Val Gln Lys Ser Pro Thr
      145             150             155             160

      Asn His Phe Pro Ser Ser Gly Arg Gly Ser Ser Lys Pro Ser Leu Leu
                  165             170             175

      Pro Lys Thr Trp Thr Glu Met Asp Ile Met Glu His Val Gly Gln Lys
                  180             185             190

      Leu Trp Asn His Lys Gly Arg Arg Val Leu Arg Leu Arg Phe Val Cys
          195             200             205

      Gln Gln Pro Arg Gly Ser Glu Val Leu Glu Phe Trp Trp His Gly Thr
          210             215             220

      Ser Ser Leu Asp Thr Val Phe Leu Leu Leu Tyr Phe Asn Asp Thr
      225             230             235
```

```
<210>   11: GDF-9B [S1] mutation
<211>   168
<212>   DNA
<213>   Ovis aries
<221>   CDS
<222>   (1)..(84)
<221>   mutation
<222>   (85)..(87)
<223>   c to t at 85 of [S1] sheep changes glutamine cag codon to tag
STOP

<400>   11
aga ggt agt gag gtt ctt gag ttc tgg tgg cat ggc act tca tca ttg
48
Arg Gly Ser Glu Val Leu Glu Phe Trp Trp His Gly Thr Ser Ser Leu
1               5               10              15
```

gac act gtc ttc ttg tta ctg tat ttc aat gac act tagagtgttc
94
Asp Thr Val Phe Leu Leu Leu Tyr Phe Asn Asp Thr
                20   25

agaagaccaa acctctccct aaaggcctga aagagtttac agaaaaagac ccttctcttc
154

tcttgaggag ggct
168

<210> 12: protein GDF-9B [S1] mutation
<211> 28
<212> PRT
<213> Ovis aries

<400> 12

Arg Gly Ser Glu Val Leu Glu Phe Trp Trp His Gly Thr Ser Ser Leu
1   5   10   15

Asp Thr Val Phe Leu Leu Leu Tyr Phe Asn Asp Thr
                20   25

<210> 13: GDF-9B [S2] full
<211> 1665
<212> DNA
<213> Ovis aries
<221> 5'UTR
<222> (1)..(252)
<221> misc_feature
<222> (253)..(255)
<223> atg start codon.
<221> CDS
<222> (253)..(577)
<221> CDS
<222> (774)..(1627)
<221> Intron
<222> (578)..(773)
<223> n at 685 represents approx 5.2 kb intron.
<221> mat_peptide
<222> (1253)..()
<221> misc_feature
<222> (685)..()
<223> n represents approx 5.2 kb of intron
<221> misc_feature
<222> (1628)..(1630)
<223> tga stop codon.
<221> 3'UTR
<222> (1628)..(1665)
<221> mutation
<222> (1547)..(1549)
<223>. g to t at 1548 of [S2] sheep changes agc serine codon to atc
isoleucine codon

<400> 13
catgctgcct tgtcccacct gctgtttctg tttgtttgat gcaaagagga caatttagaa
60

gacctctttt tggttcagga gatcctacca gaggaagaaa cataggacct gcctgccagc
120

ctttcatttt tccttgccct atcctttgtg gtagtggagc ctggatgctg ttacccatgt
180

aaaaggaaag gtttaaagcg ttatcctttg gcttttatc agaacatgtt gctgaacacc
240

aagcttttca ag atg gtc ctc ctg agc atc ctt aga atc ctt ctt tgg
288
            Met Val Leu Leu Ser Ile Leu Arg Ile Leu Leu Trp
                      -265   -260

gga ctg gtg ctt ttt atg gaa cat agg gtc caa atg aca cag gta
333
Gly Leu Val Leu Phe Met Glu His Arg Val Gln Met Thr Gln Val
    -255   -250   -245

ggg cag ccc tct att gcc cac ctg cct gag gcc cct acc ttg ccc
378
Gly Gln Pro Ser Ile Ala His Leu Pro Glu Ala Pro Thr Leu Pro
    -240   -235   -230

ctg att cag gag ctg cta gaa gaa gcc cct ggc aag cag cag agg
423
Leu Ile Gln Glu Leu Leu Glu Glu Ala Pro Gly Lys Gln Gln Arg
    -225   -220   -215

aag ccg cgg gtc tta ggg cat ccc tta cgg tat atg ctg gag ctg
468
Lys Pro Arg Val Leu Gly His Pro Leu Arg Tyr Met Leu Glu Leu
    -210   -205   -200

tac cag cgt tca gct gac gca agt gga cac cct agg gaa aac cgc
513
Tyr Gln Arg Ser Ala Asp Ala Ser Gly His Pro Arg Glu Asn Arg
    -195   -190   -185

acc att ggg gcc acc atg gtg agg ctg gtg agg ccg ctg gct agt
558
Thr Ile Gly Ala Thr Met Val Arg Leu Val Arg Pro Leu Ala Ser
    -180   -175   -170

gta gca agg cct ctc aga g gtgagttatc atactatatt gttctggtgg
607
Val Ala Arg Pro Leu Arg
    -165

gagggggga gaaatgggg aagaaaagtg tagaaaaag tggatctgtc agttttctgt
667

caggcttcac attgcctnca gtttgtactg agcaggtctg ttagagagac taaggctagg
727

atataagaag ctaacgcttt gctcttgttc cctcttacta atgcag gc   tcc tgg
781
                                              Gly Ser Trp
                                              -160

cac ata cag acc ctg gac ttt cct ctg aga cca aac cgg gta gca
826

```
          His Ile Gln  Thr Leu Asp Phe Pro  Leu Arg Pro Asn Arg  Val Ala
                  -155             -150              -145

    5     tac caa cta gtc aga gcc act gtg gtt tac cgc cat cag ctt cac
          871
          Tyr Gln Leu  Val Arg Ala Thr Val  Val Tyr Arg His Gln  Leu His
                  -140             -135              -130

   10     cta act cat tcc cac ctc tcc tgc cat gtg gag ccc tgg gtc cag
          916
          Leu Thr His  Ser His Leu Ser Cys  His Val Glu Pro Trp  Val Gln
                  -125             -120              -115

   15     aaa agc cca acc aat cac ttt cct tct tca gga aga ggc tcc tca
          961
          Lys Ser Pro  Thr Asn His Phe Pro  Ser Ser Gly Arg Gly  Ser Ser
                  -110             -105              -100

   20     aag cct tcc ctg ttg ccc aaa act tgg aca gag atg gat atc atg gaa
          1009
          Lys Pro Ser  Leu Leu Pro Lys Thr  Trp Thr Glu Met Asp  Ile Met Glu
                  -95              -90               -85

   25     cat gtt ggg caa aag ctc tgg aat cac aag ggg cgc agg gtt cta cga
          1057
          His Val Gly  Gln Lys Leu Trp Asn  His Lys Gly Arg Arg  Val Leu Arg
                  -80              -75               -70

   30     ctc cgc ttc gtg tgt cag cag cca aga ggt agt gag gtt ctt gag ttc
          1105
          Leu Arg Phe  Val Cys Gln Gln Pro  Arg Gly Ser Glu Val  Leu Glu Phe
          -65              -60               -55                -50

   35     tgg tgg cat ggc act tca tca ttg gac act gtc ttc ttg tta ctg tat
          1153
          Trp Trp His  Gly Thr Ser Ser Leu  Asp Thr Val Phe Leu  Leu Leu Tyr
                  -45              -40               -35

   40     ttc aat gac act cag agt gtt cag aag acc aaa cct ctc cct aaa ggc
          1201
          Phe Asn Asp  Thr Gln Ser Val Gln  Lys Thr Lys Pro Leu  Pro Lys Gly
                  -30              -25               -20

   45     ctg aaa gag ttt aca gaa aaa gac cct tct ctt ctc ttg agg agg gct
          1249
          Leu Lys Glu  Phe Thr Glu Lys Asp  Pro Ser Leu Leu Leu  Arg Arg Ala
                  -15              -10               -5

   50     cgt caa gca ggc agt att gca tcg gaa gtt cct ggc ccc tcc agg gag
          1297
          Arg Gln Ala  Gly Ser Ile Ala Ser  Glu Val Pro Gly Pro  Ser Arg Glu
          -1  1             5                10                 15

   55     cat gat ggg cct gaa agt aac cag tgt tcc ctc cac cct ttt caa gtc
          1345
          His Asp Gly  Pro Glu Ser Asn Gln  Cys Ser Leu His Pro  Phe Gln Val
                  20               25                30

   60     agc ttc cag cag ctg ggc tgg gat cac tgg atc att gct ccc cat ctc
          1393
          Ser Phe Gln  Gln Leu Gly Trp Asp  His Trp Ile Ile Ala  Pro His Leu
                  35               40                45
```

```
tat acc cca aac tac tgt aag gga gta tgt cct cgg gta cta cac tat
1441
Tyr Thr Pro Asn Tyr Cys Lys Gly Val Cys Pro Arg Val Leu His Tyr
        50                  55                  60

ggt ctc aat tct ccc aat cat gcc atc atc cag aac ctt gtc agt gag
1489
Gly Leu Asn Ser Pro Asn His Ala Ile Ile Gln Asn Leu Val Ser Glu
        65                  70                  75

ctg gtg gat cag aat gtc cct cag cct tcc tgt gtc cct tat aag tat
1537
Leu Val Asp Gln Asn Val Pro Gln Pro Ser Cys Val Pro Tyr Lys Tyr
80                  85                  90                  95

gtt ccc att atc atc ctt ctg att gag gca aat ggg agt atc ttg tac
1585
Val Pro Ile Ile Ile Leu Leu Ile Glu Ala Asn Gly Ser Ile Leu Tyr
                100                 105                 110

aag gag tat gag ggt atg att gcc cag tcc tgc aca tgc agg
1627
Lys Glu Tyr Glu Gly Met Ile Ala Gln Ser Cys Thr Cys Arg
            115                 120                 125

tgacggcaaa ggtgcagcta gctcaggttt cccaagaa
1665
```

```
<210>  14: protein GDF-9B [S1] mutation
<211>  393
<212>  PRT
<213>  Ovis aries
<221>  misc_feature
<222>  (253)..(255)
<223>  atg start codon.
<221>  misc_feature
<222>  (685)..()
<223>  n represents approx 5.2 kb of intron
<221>  misc_feature
<222>  (1628)..(1630)
<223>  tga stop codon.

<400>  14
```

```
Met Val Leu Leu  Ser Ile Leu Arg  Ile  Leu Leu Trp Gly Leu  Val
            -265                 -260                 -255


Leu Phe Met Glu  His Arg Val Gln  Met  Thr Gln Val Gly Gln  Pro
            -250                 -245                 -240


Ser Ile Ala His  Leu Pro Glu Ala  Pro  Thr Leu Pro Leu Ile  Gln
            -235                 -230                 -225


Glu Leu Leu Glu  Glu Ala Pro Gly  Lys  Gln Gln Arg Lys Pro  Arg
            -220                 -215                 -210


Val Leu Gly His  Pro Leu Arg Tyr  Met  Leu Glu Leu Tyr Gln  Arg
            -205                 -200                 -195
```

```
5          Ser Ala Asp Ala  Ser Gly His Pro Arg  Glu Asn Arg Thr Ile  Gly
                   -190                  -185                 -180

           Ala Thr Met Val  Arg Leu Val Arg Pro  Leu Ala Ser Val Ala  Arg
10                 -175                  -170                 -165

           Pro Leu Arg Gly  Ser Trp His Ile Gln  Thr Leu Asp Phe Pro  Leu
15                 -160                  -155                 -150

           Arg Pro Asn Arg  Val Ala Tyr Gln Leu  Val Arg Ala Thr Val  Val
20                 -145                  -140                 -135

           Tyr Arg His Gln  Leu His Leu Thr His  Ser His Leu Ser Cys  His
                   -130                  -125                 -120

           Val Glu Pro Trp  Val Gln Lys Ser Pro  Thr Asn His Phe Pro  Ser
25                 -115                  -110                 -105

           Ser Gly Arg Gly  Ser Ser Lys Pro Ser  Leu Leu Pro Lys Thr  Trp Thr
30                 -100                  -95                  -90

           Glu Met Asp Ile Met Glu His Val  Gly Gln Lys Leu Trp Asn  His Lys
                   -85                  -80                   -75

           Gly Arg Arg Val Leu Arg Leu Arg  Phe Val Cys Gln Gln Pro  Arg Gly
35                 -70                  -65                   -60

           Ser Glu Val Leu Glu Phe Trp Trp  His Gly Thr Ser Ser Leu  Asp Thr
40         -55                -50                  -45                   -40

           Val Phe Leu Leu Leu Tyr Phe Asn  Asp Thr Gln Ser Val Gln  Lys Thr
45                 -35                  -30                   -25

           Lys Pro Leu Pro Lys Gly Leu Lys  Glu Phe Thr Glu Lys Asp  Pro Ser
                   -20                  -15                   -10

50         Leu Leu Leu Arg Arg Ala Arg Gln  Ala Gly Ser Ile Ala Ser  Glu Val
                   -5                   -1  1                 5

           Pro Gly Pro Ser Arg Glu His Asp  Gly Pro Glu Ser Asn Gln  Cys Ser
55         10                 15                   20                    25

           Leu His Pro Phe Gln Val Ser Phe  Gln Gln Leu Gly Trp Asp  His Trp
60                 30                   35                    40
```

```
Ile Ile Ala Pro His Leu Tyr Thr Pro Asn Tyr Cys Lys Gly Val Cys
            45                  50              55
```

```
Pro Arg Val Leu His Tyr Gly Leu Asn Ser Pro Asn His Ala Ile Ile
            60                  65              70
```

```
Gln Asn Leu Val Ser Glu Leu Val Asp Gln Asn Val Pro Gln Pro Ser
            75                  80              85
```

```
Cys Val Pro Tyr Lys Tyr Val Pro Ile Ile Ile Leu Leu Ile Glu Ala
90                  95              100                 105
```

```
Asn Gly Ser Ile Leu Tyr Lys Glu Tyr Glu Gly Met Ile Ala Gln Ser
            110                 115             120
```

```
Cys Thr Cys Arg
            125
```

```
<210>  15: GDF-9B [S2] coding
<211>  1182
<212>  DNA
<213>  Ovis aries
<221>  misc_feature
<222>  (1)..(3)
<223>  atg start codon.
<221>  mutation
<222>  (1099)..(1101)
<223>  g to to at 1100 of [S2] sheep changes agc serine codon to atc
isoleucine codon
<221>  CDS
<222>  (1)..(1179)
<221>  mat_peptide
<222>  (805)..()
<221>  misc_feature
<222>  (1180)..(1182)
<223>  tga stop codon.
```

```
<400>  15
atg gtc ctc ctg  agc atc ctt aga atc  ctt ctt tgg gga ctg  gtg
45
Met Val Leu Leu  Ser Ile Leu Arg Ile  Leu Leu Trp Gly Leu  Val
            -265                 -260                 -255
```

```
ctt ttt atg gaa  cat agg gtc caa atg  aca cag gta ggg cag  ccc
90
Leu Phe Met Glu  His Arg Val Gln Met  Thr Gln Val Gly Gln  Pro
            -250                 -245                 -240
```

```
tct att gcc cac  ctg cct gag gcc cct  acc ttg ccc ctg att  cag
135
Ser Ile Ala His  Leu Pro Glu Ala Pro  Thr Leu Pro Leu Ile  Gln
            -235                 -230                 -225
```

```
gag ctg cta gaa  gaa gcc cct ggc aag  cag cag agg aag ccg  cgg
180
Glu Leu Leu Glu  Glu Ala Pro Gly Lys  Gln Gln Arg Lys Pro  Arg
```

```
                    -220                    -215                    -210

        gtc tta ggg cat   ccc tta cgg tat   atg ctg gag ctg tac   cag cgt
        225
   5    Val Leu Gly His   Pro Leu Arg Tyr   Met Leu Glu Leu Tyr   Gln Arg
                      -205                -200                -195


        tca gct gac gca   agt gga cac cct   agg gaa aac cgc acc   att ggg
        270
  10    Ser Ala Asp Ala   Ser Gly His Pro   Arg Glu Asn Arg Thr   Ile Gly
                      -190                -185                -180


        gcc acc atg gtg   agg ctg gtg agg   ccg ctg gct agt gta   gca agg
        315
  15    Ala Thr Met Val   Arg Leu Val Arg   Pro Leu Ala Ser Val   Ala Arg
                      -175                -170                -165


        cct ctc aga ggc   tcc tgg cac ata   cag acc ctg gac ttt   cct ctg
        360
  20    Pro Leu Arg Gly   Ser Trp His Ile   Gln Thr Leu Asp Phe   Pro Leu
                      -160                -155                -150


        aga cca aac cgg   gta gca tac caa   cta gtc aga gcc act   gtg gtt
        405
  25    Arg Pro Asn Arg   Val Ala Tyr Gln   Leu Val Arg Ala Thr   Val Val
                      -145                -140                -135


        tac cgc cat cag   ctt cac cta act   cat tcc cac ctc tcc   tgc cat
        450
  30    Tyr Arg His Gln   Leu His Leu Thr   His Ser His Leu Ser   Cys His
                      -130                -125.               -120


        gtg gag ccc tgg   gtc cag aaa agc   cca acc aat cac ttt   cct tct
        495
  35    Val Glu Pro Trp   Val Gln Lys Ser   Pro Thr Asn His Phe   Pro Ser
                      -115                -110                -105


        tca gga aga ggc   tcc tca aag cct   tcc ctg ttg ccc aaa act tgg aca
        543
  40    Ser Gly Arg Gly   Ser Ser Lys Pro   Ser Leu Leu Pro Lys Thr Trp Thr
                      -100                -95                  -90


        gag atg gat atc   atg gaa cat gtt   ggg caa aag ctc tgg aat cac aag
        591
  45    Glu Met Asp Ile   Met Glu His Val   Gly Gln Lys Leu Trp Asn His Lys
                  -85                    -80                  -75


        ggg cgc agg gtt   cta cga ctc cgc   ttc gtg tgt cag cag cca aga ggt
        639
  50    Gly Arg Arg Val   Leu Arg Leu Arg   Phe Val Cys Gln Gln Pro Arg Gly
              -70                        -65                  -60


        agt gag gtt ctt   gag ttc tgg tgg   cat ggc act tca tca ttg gac act
        687
  55    Ser Glu Val Leu   Glu Phe Trp Trp   His Gly Thr Ser Ser Leu Asp Thr
        -55                    -50                -45                    -40


        gtc ttc ttg tta   ctg tat ttc aat   gac act cag agt gtt cag aag acc
        735
  60    Val Phe Leu Leu   Leu Tyr Phe Asn   Asp Thr Gln Ser Val Gln Lys Thr
                      -35                -30                  -25
```

```
aaa cct ctc cct aaa ggc ctg aaa gag ttt aca gaa aaa gac cct tct
783
Lys Pro Leu Pro Lys Gly Leu Lys Glu Phe Thr Glu Lys Asp Pro Ser
            -20               -15               -10

ctt ctc ttg agg agg gct cgt caa gca ggc agt att gca tcg gaa gtt
831
Leu Leu Leu Arg Arg Ala Arg Gln Ala Gly Ser Ile Ala Ser Glu Val
        -5              -1  1               5

cct ggc ccc tcc agg gag cat gat ggg cct gaa agt aac cag tgt tcc
879
Pro Gly Pro Ser Arg Glu His Asp Gly Pro Glu Ser Asn Gln Cys Ser
10                  15              20                  25

ctc cac cct ttt caa gtc agc ttc cag cag ctg ggc tgg gat cac tgg
927
Leu His Pro Phe Gln Val Ser Phe Gln Gln Leu Gly Trp Asp His Trp
                30              35                  40

atc att gct ccc cat ctc tat acc cca aac tac tgt aag gga gta tgt
975
Ile Ile Ala Pro His Leu Tyr Thr Pro Asn Tyr Cys Lys Gly Val Cys
            45              50              55

cct cgg gta cta cac tat ggt ctc aat tct ccc aat cat gcc atc atc
1023
Pro Arg Val Leu His Tyr Gly Leu Asn Ser Pro Asn His Ala Ile Ile
        60                  65              70

cag aac ctt gtc agt gag ctg gtg gat cag aat gtc cct cag cct tcc
1071
Gln Asn Leu Val Ser Glu Leu Val Asp Gln Asn Val Pro Gln Pro Ser
    75                  80                  85

tgt gtc cct tat aag tat gtt ccc att atc atc ctt ctg att gag gca
1119
Cys Val Pro Tyr Lys Tyr Val Pro Ile Ile Ile Leu Leu Ile Glu Ala
90                  95                  100                 105

aat ggg agt atc ttg tac aag gag tat gag ggt atg att gcc cag tcc
1167
Asn Gly Ser Ile Leu Tyr Lys Glu Tyr Glu Gly Met Ile Ala Gln Ser
                110                 115                 120

tgc aca tgc agg tga
1182
Cys Thr Cys Arg
                125
```

```
<210>  16: protein GDF-9B [S2] coding
<211>  393
<212>  PRT
<213>  Ovis aries
<221>  misc_feature
<222>  (1)..(3)
<223>  atg start codon.
<221>  misc_feature
<222>  (1180)..(1182)
<223>  tga stop codon.

<400>  16
```

```
          Met Val Leu Leu  Ser Ile Leu Arg Ile  Leu Leu Trp Gly Leu  Val
                   -265              -260                  -255

  5

          Leu Phe Met Glu  His Arg Val Gln Met  Thr Gln Val Gly Gln  Pro
                   -250              -245                  -240


 10       Ser Ile Ala His  Leu Pro Glu Ala Pro  Thr Leu Pro Leu Ile  Gln
                   -235              -230                  -225


          Glu Leu Leu Glu  Glu Ala Pro Gly Lys  Gln Gln Arg Lys Pro  Arg
 15                -220              -215                  -210


          Val Leu Gly His  Pro Leu Arg Tyr Met  Leu Glu Leu Tyr Gln  Arg
                   -205              -200                  -195
 20

          Ser Ala Asp Ala  Ser Gly His Pro Arg  Glu Asn Arg Thr Ile  Gly
                   -190              -185                  -180

 25
          Ala Thr Met Val  Arg Leu Val Arg Pro  Leu Ala Ser Val Ala  Arg
                   -175              -170                  -165


 30       Pro Leu Arg Gly  Ser Trp His Ile Gln  Thr Leu Asp Phe Pro  Leu
                   -160              -155                  -150


          Arg Pro Asn Arg  Val Ala Tyr Gln Leu  Val Arg Ala Thr Val  Val
 35                -145              -140                  -135


          Tyr Arg His Gln  Leu His Leu Thr His  Ser His Leu Ser Cys  His
                   -130              -125                  -120
 40

          Val Glu Pro Trp  Val Gln Lys Ser Pro  Thr Asn His Phe Pro  Ser
                   -115              -110                  -105

 45
          Ser Gly Arg Gly  Ser Ser Lys Pro Ser  Leu Leu Pro Lys Thr Trp Thr
                   -100              -95                   -90


 50       Glu Met Asp Ile  Met Glu His Val Gly  Gln Lys Leu Trp Asn His Lys
                   -85               -80                   -75


          Gly Arg Arg Val  Leu Arg Leu Arg Phe  Val Cys Gln Gln Pro Arg Gly
 55            -70               -65                   -60


          Ser Glu Val Leu  Glu Phe Trp Trp His  Gly Thr Ser Ser Leu Asp  Thr
          -55                -50                  -45                   -40
 60

          Val Phe Leu Leu  Leu Tyr Phe Asn Asp  Thr Gln Ser Val Gln Lys  Thr
                   -35               -30                   -25
```

```
         Lys Pro Leu Pro Lys Gly Leu Lys Glu Phe Thr Glu Lys Asp Pro Ser
                     -20             -15             -10

         Leu Leu Leu Arg Arg Ala Arg Gln Ala Gly Ser Ile Ala Ser Glu Val
                 -5              -1  1                   5

         Pro Gly Pro Ser Arg Glu His Asp Gly Pro Glu Ser Asn Gln Cys Ser
         10              15              20                      25

         Leu His Pro Phe Gln Val Ser Phe Gln Gln Leu Gly Trp Asp His Trp
                     .   30              35                      40

         Ile Ile Ala Pro His Leu Tyr Thr Pro Asn Tyr Cys Lys Gly Val Cys
                     45              50                      55

         Pro Arg Val Leu His Tyr Gly Leu Asn Ser Pro Asn His Ala Ile Ile
                 60              65              70

         Gln Asn Leu Val Ser Glu Leu Val Asp Gln Asn Val Pro Gln Pro Ser
             75              80                  85

         Cys Val Pro Tyr Lys Tyr Val Pro Ile Ile Ile Leu Leu Ile Glu Ala
         90              95              100                     105

         Asn Gly Ser Ile Leu Tyr Lys Glu Tyr Glu Gly Met Ile Ala Gln Ser
                         110             115                     120

         Cys Thr Cys Arg
                     125


         <210>  17: GDF-9B [S2] mutation
         <211>  168
         <212>  DNA
         <213>  Ovis aries
         <221>  CDS
         <222>  (1)..(168)
         <221>  mutation
         <222>  (85)..(87)
         <223>  g to t at 86 of GDF9B sheep changes agc serine codon to atc
         isoleucine codon

         <400>  17
         gcc atc atc cag aac ctt gtc agt gag ctg gtg gat cag aat gtc cct
         48
         Ala Ile Ile Gln Asn Leu Val Ser Glu Leu Val Asp Gln Asn Val Pro
         1               5               10                  15

         cag cct tcc tgt gtc cct tat aag tat gtt ccc att atc atc ctt ctg
         96
         Gln Pro Ser Cys Val Pro Tyr Lys Tyr Val Pro Ile Ile Ile Leu Leu
                     20              25              30
```

```
    att gag gca aat ggg agt atc ttg tac aag gag tat gag ggt atg att
    144
    Ile Glu Ala Asn Gly Ser Ile Leu Tyr Lys Glu Tyr Glu Gly Met Ile
            35                  40                  45

    gcc cag tcc tgc aca tgc agg tga
    168
    Ala Gln Ser Cys Thr Cys Arg
        50                  55
```

<210> 18: protein GDF-9B [S2] coding
<211> 55
<212> PRT
<213> Ovis aries

<400> 18

```
Ala Ile Ile Gln Asn Leu Val Ser Glu Leu Val Asp Gln Asn Val Pro
1               5                   10                  15


Gln Pro Ser Cys Val Pro Tyr Lys Tyr Val Pro Ile Ile Ile Leu Leu
            20    .            25                  30


Ile Glu Ala Asn Gly Ser Ile Leu Tyr Lys Glu Tyr Glu Gly Met Ile
        35                  40                  45


Ala Gln Ser Cys Thr Cys Arg
    50                  55
```